

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: SANOFI
 (B) STREET: 32,34 rue MARBEUF
 (C) CITY: PARIS
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE (ZIP): 75374
 (G) TELEPHONE: 0153774000
 (H) TELEFAX: 0153774133

(ii) TITLE OF INVENTION: IL-13 receptor

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: Carcinoma
 (G) CELL TYPE: renal
 (H) CELL LINE: caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTGCCTGTC GGCAGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AAATGGCTTA	60
ATTCGTTTGC TTGGCTATCG GATGCTTATA TACCTTTCTG ATAAGCACAA CATTTGGCTG	120
TACAAGCTTT TGCAC TTCAT CTTCAGACAC CGAGATAAAA GTTAACCCTC CTCAGGATTT	180
TGAGATAGTG GATTATGAAG AGAACCCGGA TACTTAGGTT ATCTCTATTT GCAATGGCAA	240
CCCCCACTGT CTCTGGATCA TTTGTGTGTTG TGAAAGGAAT GCACAGTGGA ATATGAAC TA	300
AAATACCGAA ACATTGGTAG TGAAACATGG AAGGCTAGTG TAGAGGTTAC CATCATTACT	360
AAGAATCTAC ATTACAAAGA TGGGTTTGAT CTTAACAAGG GCATTGAATT ATAGAAGGGC	420
GAAGATACAC ACGCTTTTAC CATGGCAATG CACAAATGGA TCAGAAGTTC AAAGTTCCAA	480
TTGCTAGGAG TGGGCAGAAA CTACTTATTG GATATCACCA CAAGGAATTC CAGAAACTAA	540
AGTTCAGGAT TAAGTTTTTG GTAGAATGGA TTGCGTATAT TACAATTGGC AATATTTACT	600
CTGTTCTTGG AAACCTGGCA TAGGTTACAT TATGTCTGGG TACTTCTTGA TACCAATTAC	660
AACTTGTTTT ACTGGTATGA GGGCTTGGAT CATGCATTAA ATATATTTGG AAACAGTGTG	720
TTGATTACAT CAAGGCTGAT GGACAAAATA TAGGATGCAG ATTTCCCTAT TTGGCAATAA	780

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AGGAGCAGTG AGGCATCAGA CTATAAAGAT TTCTATATTT GTGTTAATGG ATCATCAGAG 840
 AACAAGCCTG AAATATCAAG GAATCAGATC CAGTTATTTT ACTTTTCAGC TTCAAAATAT 900
 AGTTAAACCT TTGCCGCCAG TCAGTTGGAA ATATCTTACT TTTACTCGGG AGAGTTCATG 960
 TGAAATTAAG CTGAAATGGA GCATACCTTT GTTTAGGCGT GGACCTATTC CAGCAAGGTG 1020
 TTTTGATTAT GAAATTGAGA TCAGAGAAGA TGATACTACC GAAAGCATGG AGGAATTTTG 1080
 GTGACTGCTA CAGTTGAAAA TGAAACATAC ACCTTGAAAA CAACAAATGA AACCCGAATA 1140
 ATAGAGTTTT TAGTAGCAAT TATGCTTTGT AGTAAGAAGC AAAGTGAATA TTTATTGCTC 1200
 AGATGACGGA ATTTGGGCAA AGAATCAAGT AGTGAGTGGA GTGATAAACA ATGCTGGGAA 1260
 GGTGAAGACC TATCGAAGAA AACTTTGCTA GTAGCTGGGA TCGTTTCTGG CTACCATTTG 1320
 GTTTCATCTT AATATTAGTT ATATTTGTAA CCGGTCTGCT TAGTGAATGT TGCGTAAAGCC 1380
 AAACACCTAC CCAAAATGA TTCCAGAATT TTTCTGTGAT ACATGAAGAA GATTTGCATC 1440
 TTTCCATATC AAGAGACATG GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA 1500
 TATGAGTCTC AATAAACTGA ATTTTCTTG CGAATGTTG 1539

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
 - (G) CELL TYPE: renal
 - (H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1 5 10 15
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45
 Leu Tyr Leu Gln Trp Gln Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125

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Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Carcinoma
- (G) CELL TYPE: RENAL
- (H) CELL LINE: Caki-1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAGCCCGGC	CGGGCTCCGA	GGCGAGAGGC	TGCATGGAGT	GGCCGGCGCG	GCTCTGCGGG	60
CTGTGGGCGC	TGCTGCTCTG	CGCCGGCGGC	GGGGGCGGGG	GCGGGGCGCG	CGCGCCTACG	120
GAAACTCAGC	CACCTGTGAC	AAATTTGAGT	GTCTCTGTTG	AAAACCTCTG	CACAGTAATA	180
TGGACATGGA	ATCCACCCGA	GGGAGCCAGC	TCAAATTGTA	GTCTATGGTA	TTTTAGTCAT	240
TTTGGCGACA	AACAAGATAA	GAAAATAGCT	CCGGAAACTC	GTCTTCAAT	AGAAGTACCC	300
CTGAATGAGA	GGATTTGTCT	GCAAGTGGGG	TCCAGTGTA	GCACCAATGA	GAGTGAGAAG	360
CCTAGCATTT	TGGTTGAAAA	ATGCATCTCA	CCCCCAGAAG	GTGATCCTGA	GTCTGCTGTG	420
ACTGAGCTTC	AATGCATTTG	GCACAACCTG	AGCTACATGA	AGTGTTCCTG	GCTCCCTGGA	480
AGGAATACCA	GTCCCGACAC	TAATACTACT	CTCTACTATT	GGCACAGAAG	CCTGGAAAAA	540
ATTCATCAAT	GTGAAAACAT	CTTTAGAGAA	GGCCAATACT	TTGGTTGTTC	CTTTGATCTG	600
ACCAAAGTGA	AGGATTCCAG	TTTTGAACAA	CACAGTGTCC	AAATAATGGT	CAAGGATAAT	660
GCAGGAAAAA	TTAAACCATC	CTTCAATATA	GTGCCTTTAA	CTTCCCGTGT	GAAACCTGAT	720
CCTCCACATA	TTAAAAACCT	CTCCTTCCAC	AATGATGACC	TATATGTGCA	ATGGGAGAAT	780
CCACAGAATT	TTATTAGCAG	ATGCCTATTT	TATGAAGTAG	AAGTCAATAA	CAGCCAAACT	840
GAGACACATA	ATGTTTTCTA	CGTCCAAGAG	GCTAAATGTG	AGAATCCAGA	ATTTGAGAGA	900
AATGTGGAGA	ATACATCTTG	TTTCATGGTC	CCTGGTGTTT	TTCCTGATAC	TTTGAACACA	960
GTCAGAATAA	GAGTCAAAAC	AAATAAGTTA	TGCTATGAGG	ATGACAAACT	CTGGAGTAAT	1020
TGGAGCCAAG	AAATGAGTAT	AGGTAAGAAG	CGCAATTCCA	CACTCTACAT	AACCATGTTA	1080
CTCATTGTTT	CAGTCATCGT	CGCAGGTGCA	ATCATAGTAC	TCCTGCTTTA	CCTAAAAAGG	1140
CTCAAGATTA	TTATATTCCC	TCCAATTCCCT	GATCCTGGCA	AGATTTTTAA	AGAAATGTTT	1200
GGAGACCAGA	ATGATGATAC	TCTGCACTGG	AAGAAGTACG	ACATCTATGA	GAAGCAAACC	1260
AAGGAGGAAA	CCGACTCTGT	AGTGCTGATA	GAAAACCTGA	AGAAAGCCTC	TCAGTGATGG	1320
AGATAATTTA	TTTTTACCTT	CACTGTGACC	TTGAGAAGAT	TCTTCCCATT	CTCCATTGTG	1380
TATCTGGGAA	CTTATTAAAT	GGAAACTGAA	ACTACTGCAC	CATTTAAAAA	CAGGCAGCTC	1440
ATAAGAGCCA	CAGGTCTTTA	TGTTGAGTCG	CGCACCAGAA	AACTAAAAAT	AATGGGCGCT	1500
TTGGAGAAGA	GTGTGGAGTC	ATTCTCATTG	AATTATAAAA	GCCAGCAGGC	TTCAAACCTAG	1560
GGGACAAAGC	AAAAAGTGAT	GATAGTGGTG	GAGTTAATCT	TATCAAGAGT	TGTGACAACCT	1620
TCCTGAGGGA	TCTATACTTG	CTTGTGTGTC	TTTGTGTCAA	CATGAACAAA	TTTTATTTGT	1680
AGGGGAACCT	ATTTGGGGTG	CAAATGCTAA	TGTCAAACCT	GAGTCACAAA	GAACATGTAG	1740
AAAACAAAAT	GGATAAAATC	TGATATGTAT	TGTTTGGGAT	CCTATTGAAC	CATGTTTGTG	1800
GCTATTAAAA	CTCTTTTAAC	AGTCTGGGCT	GGGTCCGGTG	GCTCACGCCT	GTAATCCCAG	1860
CAATTTGGGA	GTCCGAGGCG	GGCGGATCAC	TCGAGGTCAG	GAGTTCCAGA	CCAGCCTGAC	1920
CAAAATGGTG	AAACCTCCTC	TCTACTAAAA	CTACAAAAAT	TAAGTGGGTG	TGGTGGCGCG	1980
TGCCTGTAAT	CCCAGCTACT	CGGGAAGCTG	AGGCAGGTGA	ATTGTTTGAA	CCTGGGAGGT	2040

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GGAGGTTGCA	GTGAGCAGAG	ATCACACCAC	TGCACTCTAG	CCTGGGTGAC	AGAGCAAGAC	2100
TCTGTCTAAA	AAACAAAACA	AAACAAAACA	AAACAAAAAA	ACCTCTTAAT	ATTCTGGAGT	2160
CATCATTCCC	TTCGACAGCA	TTTTCTCTG	CTTTGAAAGC	CCCAGAAATC	AGTGTGGGCC	2220
ATGATGACAA	CTACAGAAAA	ACCAGAGGCA	GCTTCTTTGC	CAAGACCTTT	CAAAGCCATT	2280
TTAGGCTGTT	AGGGGCAGTG	GAGGTAGAAT	GACTCCTTGG	GTATTAGAGT	TTCAACCATG	2340
AAGTCTCTAA	CAATGTATTT	TCTTCACCTC	TGCTACTCAA	GTAGCATTTA	CTGTGTCTTT	2400
GGTTTGTGCT	AGGCCCCCGG	GTGTGAAGCA	CAGACCCCTT	CCAGGGGTTT	ACAGTCTATT	2460
TGAGACTCCT	CAGTTCTTGC	CACTTTTTTT	TTTAATCTCC	ACCAGTCATT	TTTCAGACCT	2520
TTTAACTCCT	CAATTCCAAC	ACTGATTTCC	CCTTTTGCAT	TCTCCCTCCT	TCCCTTCCTT	2580
GTAGCCTTTT	GACTTTTCATT	GGAAATTAGG	ATGTAAATCT	GCTCAGGAGA	CCTGGAGGAG	2640
CAGAGGATAA	TTAGCATCTC	AGGTTAAGTG	TGAGTAATCT	GAGAAACAAT	GACTAATTCT	2700
TGCATATTTT	GTAACCTCCA	TGTGAGGGTT	TTCAGCATTG	ATATTTGTGC	ATTTTCTAAA	2760
CAGAGATGAG	GTGGTATCTT	CACGTAGAAC	ATTGGTATTC	GCTTGAGAAA	AAAAGAATAG	2820
TTGAACCTAT	TTCTCTTTCT	TTACAAGATG	GGTCCAGGAT	TCCTCTTTTC	TCTGCCATAA	2880
ATGATTAATT	AAATAGCTTT	TGTGTCTTAC	ATTGGTAGCC	AGCCAGCCAA	GGCTCTGTTT	2940
ATGCTTTTGG	GGGGCATATA	TTGGGTTCCT	TTCTCACCTA	TCCACACAAC	ATATCCGTAT	3000
ATATCCCCTC	TACTCTTACT	TCCCCCAAAT	TTAAAGAAGT	ATGGGAAATG	AGAGGCATTT	3060
CCCCCACCCC	ATTTCTCTCC	TCACACACAG	ACTCATATTA	CTGGTAGGAA	CTTGAGAACT	3120
TTATTTCCAA	GTTGTTCAAA	CATTTACCAA	TCATATTAAT	ACAATGATGC	TATTTGCAAT	3180
TCCTGCTCCT	AGGGGAGGGG	AGATAAGAAA	CCCTCACTCT	CTACAGGTTT	GGGTACAAGT	3240
GGCAACCTGC	TTCCATGGCC	GTGTAGAAGC	ATGGTGCCCT	GGCTTCTCTG	AGGAAGCTGG	3300
GGTTCATGAC	AATGGCAGAT	GTAAAGTTAT	TCTTGAAGTC	AGATTGAGGC	TGGGAGACAG	3360
CCGTAGTAGA	TGTTCTACTT	TGTTCTGCTG	TTCTCTAGAA	AGAATATTTG	GTTTTCTCTG	3420
ATAGGAATGA	GATTAATTCC	TTTCCAGGTA	TTTTATAATT	CTGGGAAGCA	AAACCCATGC	3480
CTCCCCCTAG	CCATTTTTC	TGTTATCCTA	TTTAGATGGC	CATGAAGAGG	ATGCTGTGAA	3540
ATTCCCAACA	AACATTGATG	CTGACAGTCA	TGCAGTCTGG	GAGTGGGGAA	GTGATCTTTT	3600
GTTCCCATCC	TCTTCTTTTA	GCAGTAAAAT	AGCTGAGGGA	AAAGGGAGGG	AAAAGGAAGT	3660
TATGGGAATA	CCTGTGGTGG	TTGTGATCCC	TAGGTCTTGG	GAGCTCTTGG	AGGTGTCTGT	3720
ATCAGTGGAT	TTCCCATCCC	CTGTGGGAAA	TTAGTAGGCT	CATTTACTGT	TTTAGGTCTA	3780
GCCTATGTGG	ATTTTTTTCCT	AACATACCTA	AGCAAACCCA	GTGTCAGGAT	GGTAATTCTT	3840
ATTCTTTCGT	TCAGTTAAGT	TTTCCCTTC	ATCTGGGCAC	TGAAGGGATA	TGTGAAACAA	3900
TGTTAACATT	TTTGGTAGTC	TTCAACCAGG	GATTGTTTCT	GTTTAACTTC	TTATAGGAAA	3960
GCTTGAGTAA	AATAAATATT	GTCTTTTTGT	ATGTCACCCA	AAAAAAAAA		4009

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: Carcinoma
 (G) CELL TYPE: renal
 (H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
 20 25 30
 Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
 35 40 45
 Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
 50 55 60
 Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
 65 70 75 80
 Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
 85 90 95
 Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
 100 105 110
 Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
 115 120 125
 Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
 130 135 140
 Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
 145 150 155 160
 Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
 165 170 175
 Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
 180 185 190
 Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
 195 200 205
 Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
 210 215 220
 Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
 225 230 235 240
 Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
 245 250 255
 Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
 260 265 270
 Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
 275 280 285

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Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
 290 295 300
 Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
 305 310 315 320
 Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
 325 330 335
 Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
 340 345 350
 Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys
 355 360 365
 Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
 370 375 380
 Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
 385 390 395 400
 Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
 405 410 415
 Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425

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